

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/684,440A
Source: 1600 - EFS
Date Processed by STIC: 5-26-05

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 05/26/2005

PATENT APPLICATION: US/10/684,440A

TIME: 12:57:54

Input Set : N:\efs\10684440A_efs\ptoms.txt

Output Set: N:\CRF4\05262005\J684440A.raw

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3 <110> APPLICANT: Rosanne M. Crooke
4     Mark J. Graham
6 <120> TITLE OF INVENTION: MODULATION OF APOLIPOPROTEIN(A) EXPRESSION
8 <130> FILE REFERENCE: ISPH.0595US.P1
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/684,440A
C--> 10 <141> CURRENT FILING DATE: 2003-10-15
10 <150> PRIOR APPLICATION NUMBER: 09/923,515
11 <151> PRIOR FILING DATE: 2001-08-07
13 <150> PRIOR APPLICATION NUMBER: 60/475,402
14 <151> PRIOR FILING DATE: 2003-06-02
17 <160> NUMBER OF SEQ ID NOS: 76
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 20
21 <212> TYPE: DNA
22 <213> ORGANISM: Artificial Sequence
24 <220> FEATURE:
25 <223> OTHER INFORMATION: Antisense Oligonucleotide
27 <400> SEQUENCE: 1
28 tccgtcatcg ctctcaggg                                20
31 <210> SEQ ID NO: 2
32 <211> LENGTH: 20
33 <212> TYPE: DNA
34 <213> ORGANISM: Artificial Sequence
36 <220> FEATURE:
37 <223> OTHER INFORMATION: Antisense Oligonucleotide
39 <400> SEQUENCE: 2
40 gtgcgcgcga gcccgaaatc                                20
43 <210> SEQ ID NO: 3
44 <211> LENGTH: 20
45 <212> TYPE: DNA
46 <213> ORGANISM: Artificial Sequence
48 <220> FEATURE:
49 <223> OTHER INFORMATION: Antisense Oligonucleotide
51 <400> SEQUENCE: 3
52 atgcattctg cccccaagga                                20
55 <210> SEQ ID NO: 4
56 <211> LENGTH: 13938
57 <212> TYPE: DNA
58 <213> ORGANISM: H. sapiens
60 <220> FEATURE:
61 <221> NAME/KEY: CDS
62 <222> LOCATION: (46)...(13692)
64 <400> SEQUENCE: 4

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Input Set : N:\efs\10684440A_efs\ptoms.txt

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65 ctgggattgg gacacacttt ctggacactg ctggccagtc ccaaa atg gaa cat aag      57
66                                     Met Glu His Lys
67                                     1
69 gaa gtg gtt ctt cta ctt ctt tta ttt ctg aaa tca gca gca cct gag      105
70 Glu Val Val Leu Leu Leu Leu Phe Leu Lys Ser Ala Ala Pro Glu
71   5                10                15                20
73 caa agc cat gtg gtc cag gat tgc tac cat ggt gat gga cag agt tat      153
74 Gln Ser His Val Val Gln Asp Cys Tyr His Gly Asp Gly Gln Ser Tyr
75                25                30                35
77 cga ggc acg tac tcc acc act gtc aca gga agg acc tgc caa gct tgg      201
78 Arg Gly Thr Tyr Ser Thr Thr Val Thr Gly Arg Thr Cys Gln Ala Trp
79                40                45                50
81 tca tct atg aca cca cat caa cat aat agg acc aca gaa aac tac cca      249
82 Ser Ser Met Thr Pro His Gln His Asn Arg Thr Thr Glu Asn Tyr Pro
83                55                60                65
85 aat gct ggc ttg atc atg aac tac tgc agg aat cca gat gct gtg gca      297
86 Asn Ala Gly Leu Ile Met Asn Tyr Cys Arg Asn Pro Asp Ala Val Ala
87                70                75                80
89 gct cct tat tgt tat acg agg gat ccc ggt gtc agg tgg gag tac tgc      345
90 Ala Pro Tyr Cys Tyr Thr Arg Asp Pro Gly Val Arg Trp Glu Tyr Cys
91   85                90                95                100
93 aac ctg acg caa tgc tca gac gca gaa ggg act gcc gtc gcg cct ccg      393
94 Asn Leu Thr Gln Cys Ser Asp Ala Glu Gly Thr Ala Val Ala Pro Pro
95                105                110                115
97 act gtt acc ccg gtt cca agc cta gag gct cct tcc gaa caa gca ccg      441
98 Thr Val Thr Pro Val Pro Ser Leu Glu Ala Pro Ser Glu Gln Ala Pro
99                120                125                130
101 act gag caa agg cct ggg gtg cag gag tgc tac cat ggt aat gga cag      489
102 Thr Glu Gln Arg Pro Gly Val Gln Glu Cys Tyr His Gly Asn Gly Gln
103                135                140                145
105 agt tat cga ggc aca tac tcc acc act gtc aca gga aga acc tgc caa      537
106 Ser Tyr Arg Gly Thr Tyr Ser Thr Thr Val Thr Gly Arg Thr Cys Gln
107                150                155                160
109 gct tgg tca tct atg aca cca cac tcg cat agt cgg acc cca gaa tac      585
110 Ala Trp Ser Ser Met Thr Pro His Ser His Ser Arg Thr Pro Glu Tyr
111 165                170                175                180
113 tac cca aat gct ggc ttg atc atg aac tac tgc agg aat cca gat gct      633
114 Tyr Pro Asn Ala Gly Leu Ile Met Asn Tyr Cys Arg Asn Pro Asp Ala
115                185                190                195
117 gtg gca gct cct tat tgt tat acg agg gat ccc ggt gtc agg tgg gag      681
118 Val Ala Ala Pro Tyr Cys Tyr Thr Arg Asp Pro Gly Val Arg Trp Glu
119                200                205                210
121 tac tgc aac ctg acg caa tgc tca gac gca gaa ggg act gcc gtc gcg      729
122 Tyr Cys Asn Leu Thr Gln Cys Ser Asp Ala Glu Gly Thr Ala Val Ala
123                215                220                225
125 cct ccg act gtt acc ccg gtt cca agc cta gag gct cct tcc gaa caa      777
126 Pro Pro Thr Val Thr Pro Val Pro Ser Leu Glu Ala Pro Ser Glu Gln
127                230                235                240
129 gca ccg act gag caa agg cct ggg gtg cag gag tgc tac cat ggt aat      825

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130	Ala	Pro	Thr	Glu	Gln	Arg	Pro	Gly	Val	Gln	Glu	Cys	Tyr	His	Gly	Asn	
131	245					250					255					260	
133	gga	cag	agt	tat	cga	ggc	aca	tac	tcc	acc	act	gtc	aca	gga	aga	acc	873
134	Gly	Gln	Ser	Tyr	Arg	Gly	Thr	Tyr	Ser	Thr	Thr	Val	Thr	Gly	Arg	Thr	
135					265					270						275	
137	tgc	caa	gct	tgg	tca	tct	atg	aca	cca	cac	tcg	cat	agt	cgg	acc	cca	921
138	Cys	Gln	Ala	Trp	Ser	Ser	Met	Thr	Pro	His	Ser	His	Ser	Arg	Thr	Pro	
139					280					285						290	
141	gaa	tac	tac	cca	aat	gct	ggc	ttg	atc	atg	aac	tac	tgc	agg	aat	cca	969
142	Glu	Tyr	Tyr	Pro	Asn	Ala	Gly	Leu	Ile	Met	Asn	Tyr	Cys	Arg	Asn	Pro	
143					295				300							305	
145	gat	gct	gtg	gca	gct	cct	tat	tgt	tat	acg	agg	gat	ccc	ggt	gtc	agg	1017
146	Asp	Ala	Val	Ala	Ala	Pro	Tyr	Cys	Tyr	Thr	Arg	Asp	Pro	Gly	Val	Arg	
147		310						315					320				
149	tgg	gag	tac	tgc	aac	ctg	acg	caa	tgc	tca	gac	gca	gaa	ggg	act	gcc	1065
150	Trp	Glu	Tyr	Cys	Asn	Leu	Thr	Gln	Cys	Ser	Asp	Ala	Glu	Gly	Thr	Ala	
151	325					330					335					340	
153	gtc	gcg	cct	ccg	act	ggt	acc	ccg	ggt	cca	agc	cta	gag	gct	cct	tcc	1113
154	Val	Ala	Pro	Pro	Thr	Val	Thr	Pro	Val	Pro	Ser	Leu	Glu	Ala	Pro	Ser	
155					345					350						355	
157	gaa	caa	gca	ccg	act	gag	caa	agg	cct	ggg	gtg	cag	gag	tgc	tac	cat	1161
158	Glu	Gln	Ala	Pro	Thr	Glu	Gln	Arg	Pro	Gly	Val	Gln	Glu	Cys	Tyr	His	
159					360					365						370	
161	ggt	aat	gga	cag	agt	tat	cga	ggc	aca	tac	tcc	acc	act	gtc	aca	gga	1209
162	Gly	Asn	Gly	Gln	Ser	Tyr	Arg	Gly	Thr	Tyr	Ser	Thr	Thr	Val	Thr	Gly	
163					375				380							385	
165	aga	acc	tgc	caa	gct	tgg	tca	tct	atg	aca	cca	cac	tcg	cat	agt	cgg	1257
166	Arg	Thr	Cys	Gln	Ala	Trp	Ser	Ser	Met	Thr	Pro	His	Ser	His	Ser	Arg	
167		390						395					400				
169	acc	cca	gaa	tac	tac	cca	aat	gct	ggc	ttg	atc	atg	aac	tac	tgc	agg	1305
170	Thr	Pro	Glu	Tyr	Tyr	Pro	Asn	Ala	Gly	Leu	Ile	Met	Asn	Tyr	Cys	Arg	
171	405					410					415					420	
173	aat	cca	gat	gct	gtg	gca	gct	cct	tat	tgt	tat	acg	agg	gat	ccc	ggt	1353
174	Asn	Pro	Asp	Ala	Val	Ala	Ala	Pro	Tyr	Cys	Tyr	Thr	Arg	Asp	Pro	Gly	
175					425					430						435	
177	gtc	agg	tgg	gag	tac	tgc	aac	ctg	acg	caa	tgc	tca	gac	gca	gaa	ggg	1401
178	Val	Arg	Trp	Glu	Tyr	Cys	Asn	Leu	Thr	Gln	Cys	Ser	Asp	Ala	Glu	Gly	
179					440					445						450	
181	act	gcc	gtc	gcg	cct	ccg	act	ggt	acc	ccg	ggt	cca	agc	cta	gag	gct	1449
182	Thr	Ala	Val	Ala	Pro	Pro	Thr	Val	Thr	Pro	Val	Pro	Ser	Leu	Glu	Ala	
183					455					460						465	
185	cct	tcc	gaa	caa	gca	ccg	act	gag	caa	agg	cct	ggg	gtg	cag	gag	tgc	1497
186	Pro	Ser	Glu	Gln	Ala	Pro	Thr	Glu	Gln	Arg	Pro	Gly	Val	Gln	Glu	Cys	
187		470						475					480				
189	tac	cat	ggt	aat	gga	cag	agt	tat	cga	ggc	aca	tac	tcc	acc	act	gtc	1545
190	Tyr	His	Gly	Asn	Gly	Gln	Ser	Tyr	Arg	Gly	Thr	Tyr	Ser	Thr	Thr	Val	
191	485					490					495					500	
193	aca	gga	aga	acc	tgc	caa	gct	tgg	tca	tct	atg	aca	cca	cac	tcg	cat	1593
194	Thr	Gly	Arg	Thr	Cys	Gln	Ala	Trp	Ser	Ser	Met	Thr	Pro	His	Ser	His	

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195				505				510				515					
197	agt	cgg	acc	cca	gaa	tac	tac	cca	aat	gct	ggc	ttg	atc	atg	aac	tac	1641
198	Ser	Arg	Thr	Pro	Glu	Tyr	Tyr	Pro	Asn	Ala	Gly	Leu	Ile	Met	Asn	Tyr	
199				520				525				530					
201	tgc	agg	aat	cca	gat	gct	gtg	gca	gct	cct	tat	tgt	tat	acg	agg	gat	1689
202	Cys	Arg	Asn	Pro	Asp	Ala	Val	Ala	Ala	Pro	Tyr	Cys	Tyr	Thr	Arg	Asp	
203			535					540				545					
205	ccc	ggt	gtc	agg	tgg	gag	tac	tgc	aac	ctg	acg	caa	tgc	tca	gac	gca	1737
206	Pro	Gly	Val	Arg	Trp	Glu	Tyr	Cys	Asn	Leu	Thr	Gln	Cys	Ser	Asp	Ala	
207		550					555					560					
209	gaa	ggg	act	gcc	gtc	gcg	cct	ccg	act	gtt	acc	ccg	gtt	cca	agc	cta	1785
210	Glu	Gly	Thr	Ala	Val	Ala	Pro	Pro	Thr	Val	Thr	Pro	Val	Pro	Ser	Leu	
211	565					570				575				580			
213	gag	gct	cct	tcc	gaa	caa	gca	ccg	act	gag	caa	agg	cct	ggg	gtg	cag	1833
214	Glu	Ala	Pro	Ser	Glu	Gln	Ala	Pro	Thr	Glu	Gln	Arg	Pro	Gly	Val	Gln	
215			585					590				595					
217	gag	tgc	tac	cat	ggt	aat	gga	cag	agt	tat	cga	ggc	aca	tac	tcc	acc	1881
218	Glu	Cys	Tyr	His	Gly	Asn	Gly	Gln	Ser	Tyr	Arg	Gly	Thr	Tyr	Ser	Thr	
219			600					605				610					
221	act	gtc	aca	gga	aga	acc	tgc	caa	gct	tgg	tca	tct	atg	aca	cca	cac	1929
222	Thr	Val	Thr	Gly	Arg	Thr	Cys	Gln	Ala	Trp	Ser	Ser	Met	Thr	Pro	His	
223			615					620				625					
225	tcg	cat	agt	cgg	acc	cca	gaa	tac	tac	cca	aat	gct	ggc	ttg	atc	atg	1977
226	Ser	His	Ser	Arg	Thr	Pro	Glu	Tyr	Tyr	Pro	Asn	Ala	Gly	Leu	Ile	Met	
227		630					635					640					
229	aac	tac	tgc	agg	aat	cca	gat	gct	gtg	gca	gct	cct	tat	tgt	tat	acg	2025
230	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Ala	Val	Ala	Ala	Pro	Tyr	Cys	Tyr	Thr	
231	645					650				655				660			
233	agg	gat	ccc	ggt	gtc	agg	tgg	gag	tac	tgc	aac	ctg	acg	caa	tgc	tca	2073
234	Arg	Asp	Pro	Gly	Val	Arg	Trp	Glu	Tyr	Cys	Asn	Leu	Thr	Gln	Cys	Ser	
235			665					670				675					
237	gac	gca	gaa	ggg	act	gcc	gtc	gcg	cct	ccg	act	gtt	acc	ccg	gtt	cca	2121
238	Asp	Ala	Glu	Gly	Thr	Ala	Val	Ala	Pro	Pro	Thr	Val	Thr	Pro	Val	Pro	
239			680					685				690					
241	agc	cta	gag	gct	cct	tcc	gaa	caa	gca	ccg	act	gag	caa	agg	cct	ggg	2169
242	Ser	Leu	Glu	Ala	Pro	Ser	Glu	Gln	Ala	Pro	Thr	Glu	Gln	Arg	Pro	Gly	
243			695					700				705					
245	gtg	cag	gag	tgc	tac	cat	ggt	aat	gga	cag	agt	tat	cga	ggc	aca	tac	2217
246	Val	Gln	Glu	Cys	Tyr	His	Gly	Asn	Gly	Gln	Ser	Tyr	Arg	Gly	Thr	Tyr	
247		710					715					720					
249	tcc	acc	act	gtc	aca	gga	aga	acc	tgc	caa	gct	tgg	tca	tct	atg	aca	2265
250	Ser	Thr	Thr	Val	Thr	Gly	Arg	Thr	Cys	Gln	Ala	Trp	Ser	Ser	Met	Thr	
251	725					730					735				740		
253	cca	cac	tcg	cat	agt	cgg	acc	cca	gaa	tac	tac	cca	aat	gct	ggc	ttg	2313
254	Pro	His	Ser	His	Ser	Arg	Thr	Pro	Glu	Tyr	Tyr	Pro	Asn	Ala	Gly	Leu	
255			745					750				755					
257	atc	atg	aac	tac	tgc	agg	aat	cca	gat	gct	gtg	gca	gct	cct	tat	tgt	2361
258	Ile	Met	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Ala	Val	Ala	Ala	Pro	Tyr	Cys	
259			760					765				770					

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261	tat	acg	agg	gat	ccc	ggt	gtc	agg	tgg	gag	tac	tgc	aac	ctg	acg	caa	2409
262	Tyr	Thr	Arg	Asp	Pro	Gly	Val	Arg	Trp	Glu	Tyr	Cys	Asn	Leu	Thr	Gln	
263			775					780					785				
265	tgc	tca	gac	gca	gaa	ggg	act	gcc	gtc	gcg	cct	ccg	act	gtt	acc	ccg	2457
266	Cys	Ser	Asp	Ala	Glu	Gly	Thr	Ala	Val	Ala	Pro	Pro	Thr	Val	Thr	Pro	
267		790					795					800					
269	gtt	cca	agc	cta	gag	gct	cct	tcc	gaa	caa	gca	ccg	act	gag	caa	agg	2505
270	Val	Pro	Ser	Leu	Glu	Ala	Pro	Ser	Glu	Gln	Ala	Pro	Thr	Glu	Gln	Arg	
271	805					810					815					820	
273	cct	ggg	gtg	cag	gag	tgc	tac	cat	ggt	aat	gga	cag	agt	tat	cga	ggc	2553
274	Pro	Gly	Val	Gln	Glu	Cys	Tyr	His	Gly	Asn	Gly	Gln	Ser	Tyr	Arg	Gly	
275					825					830					835		
277	aca	tac	tcc	acc	act	gtc	aca	gga	aga	acc	tgc	caa	gct	tgg	tca	tct	2601
278	Thr	Tyr	Ser	Thr	Thr	Val	Thr	Gly	Arg	Thr	Cys	Gln	Ala	Trp	Ser	Ser	
279			840						845				850				
281	atg	aca	cca	cac	tcg	cat	agt	cgg	acc	cca	gaa	tac	tac	cca	aat	gct	2649
282	Met	Thr	Pro	His	Ser	His	Ser	Arg	Thr	Pro	Glu	Tyr	Tyr	Pro	Asn	Ala	
283			855					860					865				
285	ggc	ttg	atc	atg	aac	tac	tgc	agg	aat	cca	gat	gct	gtg	gca	gct	cct	2697
286	Gly	Leu	Ile	Met	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Ala	Val	Ala	Ala	Pro	
287		870				875					880						
289	tat	tgt	tat	acg	agg	gat	ccc	ggt	gtc	agg	tgg	gag	tac	tgc	aac	ctg	2745
290	Tyr	Cys	Tyr	Thr	Arg	Asp	Pro	Gly	Val	Arg	Trp	Glu	Tyr	Cys	Asn	Leu	
291	885					890					895					900	
293	acg	caa	tgc	tca	gac	gca	gaa	ggg	act	gcc	gtc	gcg	cct	ccg	act	gtt	2793
294	Thr	Gln	Cys	Ser	Asp	Ala	Glu	Gly	Thr	Ala	Val	Ala	Pro	Pro	Thr	Val	
295					905					910					915		
297	acc	ccg	gtt	cca	agc	cta	gag	gct	cct	tcc	gaa	caa	gca	ccg	act	gag	2841
298	Thr	Pro	Val	Pro	Ser	Leu	Glu	Ala	Pro	Ser	Glu	Gln	Ala	Pro	Thr	Glu	
299			920						925				930				
301	caa	agg	cct	ggg	gtg	cag	gag	tgc	tac	cat	ggt	aat	gga	cag	agt	tat	2889
302	Gln	Arg	Pro	Gly	Val	Gln	Glu	Cys	Tyr	His	Gly	Asn	Gly	Gln	Ser	Tyr	
303			935					940					945				
305	cga	ggc	aca	tac	tcc	acc	act	gtc	aca	gga	aga	acc	tgc	caa	gct	tgg	2937
306	Arg	Gly	Thr	Tyr	Ser	Thr	Thr	Val	Thr	Gly	Arg	Thr	Cys	Gln	Ala	Trp	
307		950					955				960						
309	tca	tct	atg	aca	cca	cac	tcg	cat	agt	cgg	acc	cca	gaa	tac	tac	cca	2985
310	Ser	Ser	Met	Thr	Pro	His	Ser	His	Ser	Arg	Thr	Pro	Glu	Tyr	Tyr	Pro	
311	965					970					975					980	
313	aat	gct	ggc	ttg	atc	atg	aac	tac	tgc	agg	aat	cca	gat	gct	gtg	gca	3033
314	Asn	Ala	Gly	Leu	Ile	Met	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Ala	Val	Ala	
315					985					990					995		
317	gct	cct	tat	tgt	tat	acg	agg	gat	ccc	ggt	gtc	agg	tgg	gag	tac	tgc	3081
318	Ala	Pro	Tyr	Cys	Tyr	Thr	Arg	Asp	Pro	Gly	Val	Arg	Trp	Glu	Tyr	Cys	
319			1000						1005				1010				
321	aac	ctg	acg	caa	tgc	tca	gac	gca	gaa	ggg	act	gcc	gtc	gcg	cct	ccg	3129
322	Asn	Leu	Thr	Gln	Cys	Ser	Asp	Ala	Glu	Gly	Thr	Ala	Val	Ala	Pro	Pro	
323			1015						1020				1025				
325	act	gtt	acc	ccg	gtt	cca	agc	cta	gag	gct	cct	tcc	gaa	caa	gca	ccg	3177

VERIFICATION SUMMARY

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Input Set : N:\efs\10684440A_efs\ptoms.txt

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1208 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4



IFW16

RAW SEQUENCE LISTING

DATE: 05/26/2005

PATENT APPLICATION: US/10/684,440A

TIME: 08:22:44

Input Set : N:\efs\10684440A_efs\ISPH0595USP1SEQ_amended.txt

Output Set: N:\CRF4\05262005\J684440A.raw

3 <110> APPLICANT: Rosanne M. Crooke
 4 Mark J. Graham
 6 <120> TITLE OF INVENTION: MODULATION OF APOLIPOPROTEIN(A) EXPRESSION
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 40 gtgcgcgcga gcccgaaatc 20
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 62 <222> LOCATION: (46)...(13692)
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Does Not Comply
 Corrected Diskette Needed
 See Add. final page 1

RAW SEQUENCE LISTING

DATE: 05/26/2005

PATENT APPLICATION: US/10/684,440A

TIME: 08:22:44

Input Set : N:\efs\10684440A_efs\ISPH0595USP1SEQ_amended.txt

Output Set: N:\CRF4\05262005\J684440A.raw

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66                                     Met Glu His Lys
67                                     1
69 gaa gtg gtt ctt cta ctt ctt tta ttt ctg aaa tca gca gca cct gag      105
70 Glu Val Val Leu Leu Leu Leu Leu Phe Leu Lys Ser Ala Ala Pro Glu
71   5                10                15                20
73 caa agc cat gtg gtc cag gat tgc tac cat ggt gat gga cag agt tat      153
74 Gln Ser His Val Val Gln Asp Cys Tyr His Gly Asp Gly Gln Ser Tyr
75                25                30                35
77 cga ggc acg tac tcc acc act gtc aca gga agg acc tgc caa gct tgg      201
78 Arg Gly Thr Tyr Ser Thr Thr Val Thr Gly Arg Thr Cys Gln Ala Trp
79                40                45                50
81 tca tct atg aca cca cat caa cat aat agg acc aca gaa aac tac cca      249
82 Ser Ser Met Thr Pro His Gln His Asn Arg Thr Thr Glu Asn Tyr Pro
83                55                60                65
85 aat gct ggc ttg atc atg aac tac tgc agg aat cca gat gct gtg gca      297
86 Asn Ala Gly Leu Ile Met Asn Tyr Cys Arg Asn Pro Asp Ala Val Ala
87                70                75                80
89 gct cct tat tgt tat acg agg gat ccc ggt gtc agg tgg gag tac tgc      345
90 Ala Pro Tyr Cys Tyr Thr Arg Asp Pro Gly Val Arg Trp Glu Tyr Cys
91   85                90                95                100
93 aac ctg acg caa tgc tca gac gca gaa ggg act gcc gtc gcg cct ccg      393
94 Asn Leu Thr Gln Cys Ser Asp Ala Glu Gly Thr Ala Val Ala Pro Pro
95                105                110                115
97 act gtt acc ccg gtt cca agc cta gag gct cct tcc gaa caa gca ccg      441
98 Thr Val Thr Pro Val Pro Ser Leu Glu Ala Pro Ser Glu Gln Ala Pro
99                120                125                130
101 act gag caa agg cct ggg gtg cag gag tgc tac cat ggt aat gga cag      489
102 Thr Glu Gln Arg Pro Gly Val Gln Glu Cys Tyr His Gly Asn Gly Gln
103                135                140                145
105 agt tat cga ggc aca tac tcc acc act gtc aca gga aga acc tgc caa      537
106 Ser Tyr Arg Gly Thr Tyr Ser Thr Thr Val Thr Gly Arg Thr Cys Gln
107                150                155                160
109 gct tgg tca tct atg aca cca cac tcg cat agt cgg acc cca gaa tac      585
110 Ala Trp Ser Ser Met Thr Pro His Ser His Ser Arg Thr Pro Glu Tyr
111 165                170                175                180
113 tac cca aat gct ggc ttg atc atg aac tac tgc agg aat cca gat gct      633
114 Tyr Pro Asn Ala Gly Leu Ile Met Asn Tyr Cys Arg Asn Pro Asp Ala
115                185                190                195
117 gtg gca gct cct tat tgt tat acg agg gat ccc ggt gtc agg tgg gag      681
118 Val Ala Ala Pro Tyr Cys Tyr Thr Arg Asp Pro Gly Val Arg Trp Glu
119                200                205                210
121 tac tgc aac ctg acg caa tgc tca gac gca gaa ggg act gcc gtc gcg      729
122 Tyr Cys Asn Leu Thr Gln Cys Ser Asp Ala Glu Gly Thr Ala Val Ala
123                215                220                225
125 cct ccg act gtt acc ccg gtt cca agc cta gag gct cct tcc gaa caa      777
126 Pro Pro Thr Val Thr Pro Val Pro Ser Leu Glu Ala Pro Ser Glu Gln
127                230                235                240
129 gca ccg act gag caa agg cct ggg gtg cag gag tgc tac cat ggt aat      825

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130	Ala	Pro	Thr	Glu	Gln	Arg	Pro	Gly	Val	Gln	Glu	Cys	Tyr	His	Gly	Asn	
131	245					250					255					260	
133	gga	cag	agt	tat	cga	ggc	aca	tac	tcc	acc	act	gtc	aca	gga	aga	acc	873
134	Gly	Gln	Ser	Tyr	Arg	Gly	Thr	Tyr	Ser	Thr	Thr	Val	Thr	Gly	Arg	Thr	
135					265					270						275	
137	tgc	caa	gct	tgg	tca	tct	atg	aca	cca	cac	tcg	cat	agt	cgg	acc	cca	921
138	Cys	Gln	Ala	Trp	Ser	Ser	Met	Thr	Pro	His	Ser	His	Ser	Arg	Thr	Pro	
139					280					285						290	
141	gaa	tac	tac	cca	aat	gct	ggc	ttg	atc	atg	aac	tac	tgc	agg	aat	cca	969
142	Glu	Tyr	Tyr	Pro	Asn	Ala	Gly	Leu	Ile	Met	Asn	Tyr	Cys	Arg	Asn	Pro	
143					295					300						305	
145	gat	gct	gtg	gca	gct	cct	tat	tgt	tat	acg	agg	gat	ccc	ggt	gtc	agg	1017
146	Asp	Ala	Val	Ala	Ala	Pro	Tyr	Cys	Tyr	Thr	Arg	Asp	Pro	Gly	Val	Arg	
147		310								315						320	
149	tgg	gag	tac	tgc	aac	ctg	acg	caa	tgc	tca	gac	gca	gaa	ggg	act	gcc	1065
150	Trp	Glu	Tyr	Cys	Asn	Leu	Thr	Gln	Cys	Ser	Asp	Ala	Glu	Gly	Thr	Ala	
151	325					330					335					340	
153	gtc	gcg	cct	ccg	act	gtt	acc	ccg	gtt	cca	agc	cta	gag	gct	cct	tcc	1113
154	Val	Ala	Pro	Pro	Thr	Val	Thr	Pro	Val	Pro	Ser	Leu	Glu	Ala	Pro	Ser	
155					345						350					355	
157	gaa	caa	gca	ccg	act	gag	caa	agg	cct	ggg	gtg	cag	gag	tgc	tac	cat	1161
158	Glu	Gln	Ala	Pro	Thr	Glu	Gln	Arg	Pro	Gly	Val	Gln	Glu	Cys	Tyr	His	
159					360						365					370	
161	ggt	aat	gga	cag	agt	tat	cga	ggc	aca	tac	tcc	acc	act	gtc	aca	gga	1209
162	Gly	Asn	Gly	Gln	Ser	Tyr	Arg	Gly	Thr	Tyr	Ser	Thr	Thr	Val	Thr	Gly	
163					375						380					385	
165	aga	acc	tgc	caa	gct	tgg	tca	tct	atg	aca	cca	cac	tcg	cat	agt	cgg	1257
166	Arg	Thr	Cys	Gln	Ala	Trp	Ser	Ser	Met	Thr	Pro	His	Ser	His	Ser	Arg	
167		390									395					400	
169	acc	cca	gaa	tac	tac	cca	aat	gct	ggc	ttg	atc	atg	aac	tac	tgc	agg	1305
170	Thr	Pro	Glu	Tyr	Tyr	Pro	Asn	Ala	Gly	Leu	Ile	Met	Asn	Tyr	Cys	Arg	
171	405					410					415					420	
173	aat	cca	gat	gct	gtg	gca	gct	cct	tat	tgt	tat	acg	agg	gat	ccc	ggt	1353
174	Asn	Pro	Asp	Ala	Val	Ala	Ala	Pro	Tyr	Cys	Tyr	Thr	Arg	Asp	Pro	Gly	
175					425						430					435	
177	gtc	agg	tgg	gag	tac	tgc	aac	ctg	acg	caa	tgc	tca	gac	gca	gaa	ggg	1401
178	Val	Arg	Trp	Glu	Tyr	Cys	Asn	Leu	Thr	Gln	Cys	Ser	Asp	Ala	Glu	Gly	
179					440						445					450	
181	act	gcc	gtc	gcg	cct	ccg	act	gtt	acc	ccg	gtt	cca	agc	cta	gag	gct	1449
182	Thr	Ala	Val	Ala	Pro	Pro	Thr	Val	Thr	Pro	Val	Pro	Ser	Leu	Glu	Ala	
183					455						460					465	
185	cct	tcc	gaa	caa	gca	ccg	act	gag	caa	agg	cct	ggg	gtg	cag	gag	tgc	1497
186	Pro	Ser	Glu	Gln	Ala	Pro	Thr	Glu	Gln	Arg	Pro	Gly	Val	Gln	Glu	Cys	
187		470									475					480	
189	tac	cat	ggt	aat	gga	cag	agt	tat	cga	ggc	aca	tac	tcc	acc	act	gtc	1545
190	Tyr	His	Gly	Asn	Gly	Gln	Ser	Tyr	Arg	Gly	Thr	Tyr	Ser	Thr	Thr	Val	
191	485					490					495					500	
193	aca	gga	aga	acc	tgc	caa	gct	tgg	tca	tct	atg	aca	cca	cac	tcg	cat	1593
194	Thr	Gly	Arg	Thr	Cys	Gln	Ala	Trp	Ser	Ser	Met	Thr	Pro	His	Ser	His	

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195				505				510				515					
197	agt	cgg	acc	cca	gaa	tac	tac	cca	aat	gct	ggc	ttg	atc	atg	aac	tac	1641
198	Ser	Arg	Thr	Pro	Glu	Tyr	Tyr	Pro	Asn	Ala	Gly	Leu	Ile	Met	Asn	Tyr	
199				520				525				530					
201	tgc	agg	aat	cca	gat	gct	gtg	gca	gct	cct	tat	tgt	tat	acg	agg	gat	1689
202	Cys	Arg	Asn	Pro	Asp	Ala	Val	Ala	Ala	Pro	Tyr	Cys	Tyr	Thr	Arg	Asp	
203				535				540				545					
205	ccc	ggt	gtc	agg	tgg	gag	tac	tgc	aac	ctg	acg	caa	tgc	tca	gac	gca	1737
206	Pro	Gly	Val	Arg	Trp	Glu	Tyr	Cys	Asn	Leu	Thr	Gln	Cys	Ser	Asp	Ala	
207				550				555				560					
209	gaa	ggg	act	gcc	gtc	gcg	cct	ccg	act	gtt	acc	ccg	gtt	cca	agc	cta	1785
210	Glu	Gly	Thr	Ala	Val	Ala	Pro	Pro	Thr	Val	Thr	Pro	Val	Pro	Ser	Leu	
211	565						570					575				580	
213	gag	gct	cct	tcc	gaa	caa	gca	ccg	act	gag	caa	agg	cct	ggg	gtg	cag	1833
214	Glu	Ala	Pro	Ser	Glu	Gln	Ala	Pro	Thr	Glu	Gln	Arg	Pro	Gly	Val	Gln	
215				585				590				595					
217	gag	tgc	tac	cat	ggt	aat	gga	cag	agt	tat	cga	ggc	aca	tac	tcc	acc	1881
218	Glu	Cys	Tyr	His	Gly	Asn	Gly	Gln	Ser	Tyr	Arg	Gly	Thr	Tyr	Ser	Thr	
219				600				605				610					
221	act	gtc	aca	gga	aga	acc	tgc	caa	gct	tgg	tca	tct	atg	aca	cca	cac	1929
222	Thr	Val	Thr	Gly	Arg	Thr	Cys	Gln	Ala	Trp	Ser	Ser	Met	Thr	Pro	His	
223				615				620				625					
225	tcg	cat	agt	cgg	acc	cca	gaa	tac	tac	cca	aat	gct	ggc	ttg	atc	atg	1977
226	Ser	His	Ser	Arg	Thr	Pro	Glu	Tyr	Tyr	Pro	Asn	Ala	Gly	Leu	Ile	Met	
227				630				635				640					
229	aac	tac	tgc	agg	aat	cca	gat	gct	gtg	gca	gct	cct	tat	tgt	tat	acg	2025
230	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Ala	Val	Ala	Ala	Pro	Tyr	Cys	Tyr	Thr	
231	645						650					655				660	
233	agg	gat	ccc	ggt	gtc	agg	tgg	gag	tac	tgc	aac	ctg	acg	caa	tgc	tca	2073
234	Arg	Asp	Pro	Gly	Val	Arg	Trp	Glu	Tyr	Cys	Asn	Leu	Thr	Gln	Cys	Ser	
235				665				670				675					
237	gac	gca	gaa	ggg	act	gcc	gtc	gcg	cct	ccg	act	gtt	acc	ccg	gtt	cca	2121
238	Asp	Ala	Glu	Gly	Thr	Ala	Val	Ala	Pro	Pro	Thr	Val	Thr	Pro	Val	Pro	
239				680				685				690					
241	agc	cta	gag	gct	cct	tcc	gaa	caa	gca	ccg	act	gag	caa	agg	cct	ggg	2169
242	Ser	Leu	Glu	Ala	Pro	Ser	Glu	Gln	Ala	Pro	Thr	Glu	Gln	Arg	Pro	Gly	
243				695				700				705					
245	gtg	cag	gag	tgc	tac	cat	ggt	aat	gga	cag	agt	tat	cga	ggc	aca	tac	2217
246	Val	Gln	Glu	Cys	Tyr	His	Gly	Asn	Gly	Gln	Ser	Tyr	Arg	Gly	Thr	Tyr	
247				710				715				720					
249	tcc	acc	act	gtc	aca	gga	aga	acc	tgc	caa	gct	tgg	tca	tct	atg	aca	2265
250	Ser	Thr	Thr	Val	Thr	Gly	Arg	Thr	Cys	Gln	Ala	Trp	Ser	Ser	Met	Thr	
251	725						730					735				740	
253	cca	cac	tcg	cat	agt	cgg	acc	cca	gaa	tac	tac	cca	aat	gct	ggc	ttg	2313
254	Pro	His	Ser	His	Ser	Arg	Thr	Pro	Glu	Tyr	Tyr	Pro	Asn	Ala	Gly	Leu	
255				745				750				755					
257	atc	atg	aac	tac	tgc	agg	aat	cca	gat	gct	gtg	gca	gct	cct	tat	tgt	2361
258	Ile	Met	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Ala	Val	Ala	Ala	Pro	Tyr	Cys	
259				760				765				770					

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261	tat	acg	agg	gat	ccc	ggt	gtc	agg	tgg	gag	tac	tgc	aac	ctg	acg	caa	2409
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263			775					780					785				
265	tgc	tca	gac	gca	gaa	ggg	act	gcc	gtc	gcg	cct	ccg	act	gtt	acc	ccg	2457
266	Cys	Ser	Asp	Ala	Glu	Gly	Thr	Ala	Val	Ala	Pro	Pro	Thr	Val	Thr	Pro	
267		790					795					800					
269	gtt	cca	agc	cta	gag	gct	cct	tcc	gaa	caa	gca	ccg	act	gag	caa	agg	2505
270	Val	Pro	Ser	Leu	Glu	Ala	Pro	Ser	Glu	Gln	Ala	Pro	Thr	Glu	Gln	Arg	
271	805					810					815					820	
273	cct	ggg	gtg	cag	gag	tgc	tac	cat	ggt	aat	gga	cag	agt	tat	cga	ggc	2553
274	Pro	Gly	Val	Gln	Glu	Cys	Tyr	His	Gly	Asn	Gly	Gln	Ser	Tyr	Arg	Gly	
275				825						830					835		
277	aca	tac	tcc	acc	act	gtc	aca	gga	aga	acc	tgc	caa	gct	tgg	tca	tct	2601
278	Thr	Tyr	Ser	Thr	Thr	Val	Thr	Gly	Arg	Thr	Cys	Gln	Ala	Trp	Ser	Ser	
279			840						845					850			
281	atg	aca	cca	cac	tcg	cat	agt	cgg	acc	cca	gaa	tac	tac	cca	aat	gct	2649
282	Met	Thr	Pro	His	Ser	His	Ser	Arg	Thr	Pro	Glu	Tyr	Tyr	Pro	Asn	Ala	
283			855					860					865				
285	ggc	ttg	atc	atg	aac	tac	tgc	agg	aat	cca	gat	gct	gtg	gca	gct	cct	2697
286	Gly	Leu	Ile	Met	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Ala	Val	Ala	Ala	Pro	
287		870				875						880					
289	tat	tgt	tat	acg	agg	gat	ccc	ggt	gtc	agg	tgg	gag	tac	tgc	aac	ctg	2745
290	Tyr	Cys	Tyr	Thr	Arg	Asp	Pro	Gly	Val	Arg	Trp	Glu	Tyr	Cys	Asn	Leu	
291	885					890					895					900	
293	acg	caa	tgc	tca	gac	gca	gaa	ggg	act	gcc	gtc	gcg	cct	ccg	act	gtt	2793
294	Thr	Gln	Cys	Ser	Asp	Ala	Glu	Gly	Thr	Ala	Val	Ala	Pro	Pro	Thr	Val	
295				905						910					915		
297	acc	ccg	gtt	cca	agc	cta	gag	gct	cct	tcc	gaa	caa	gca	ccg	act	gag	2841
298	Thr	Pro	Val	Pro	Ser	Leu	Glu	Ala	Pro	Ser	Glu	Gln	Ala	Pro	Thr	Glu	
299			920						925					930			
301	caa	agg	cct	ggg	gtg	cag	gag	tgc	tac	cat	ggt	aat	gga	cag	agt	tat	2889
302	Gln	Arg	Pro	Gly	Val	Gln	Glu	Cys	Tyr	His	Gly	Asn	Gly	Gln	Ser	Tyr	
303			935					940					945				
305	cga	ggc	aca	tac	tcc	acc	act	gtc	aca	gga	aga	acc	tgc	caa	gct	tgg	2937
306	Arg	Gly	Thr	Tyr	Ser	Thr	Thr	Val	Thr	Gly	Arg	Thr	Cys	Gln	Ala	Trp	
307		950					955					960					
309	tca	tct	atg	aca	cca	cac	tcg	cat	agt	cgg	acc	cca	gaa	tac	tac	cca	2985
310	Ser	Ser	Met	Thr	Pro	His	Ser	His	Ser	Arg	Thr	Pro	Glu	Tyr	Tyr	Pro	
311	965					970					975					980	
313	aat	gct	ggc	ttg	atc	atg	aac	tac	tgc	agg	aat	cca	gat	gct	gtg	gca	3033
314	Asn	Ala	Gly	Leu	Ile	Met	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Ala	Val	Ala	
315				985						990					995		
317	gct	cct	tat	tgt	tat	acg	agg	gat	ccc	ggt	gtc	agg	tgg	gag	tac	tgc	3081
318	Ala	Pro	Tyr	Cys	Tyr	Thr	Arg	Asp	Pro	Gly	Val	Arg	Trp	Glu	Tyr	Cys	
319			1000						1005					1010			
321	aac	ctg	acg	caa	tgc	tca	gac	gca	gaa	ggg	act	gcc	gtc	gcg	cct	ccg	3129
322	Asn	Leu	Thr	Gln	Cys	Ser	Asp	Ala	Glu	Gly	Thr	Ala	Val	Ala	Pro	Pro	
323			1015						1020					1025			
325	act	gtt	acc	ccg	gtt	cca	agc	cta	gag	gct	cct	tcc	gaa	caa	gca	ccg	3177

VERIFICATION SUMMARY

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Input Set : N:\efs\10684440A_efs\ISPH0595USP1SEQ_amended.txt

Output Set: N:\CRF4\05262005\J684440A.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1208 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:2056 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3
L:2059 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:76
L:2059 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3
L:2063 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:76
L:2063 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:5
L:2064 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:76
L:2064 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4

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<213> Artificial Sequence

<220>
<223> Oligomeric Compound

<220>
<221> misc_feature
<222> (3)...(21)
<223> bases at these positions are RNA

<400> 76
ttgctctccg cctgccctgg c

21

ISPH-0595US.P1 -1- PATENT

BIOL0015US.L -1- PATENT

"Express Mail" Label No.: filed LTS
Date of Deposit: _____

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